

Table III

Totals:

Totals:

Table IV (1 of 2)

GENE DESCRIPTION	HOMOLOG ID	SNP ID	CONTROL POS	FLANK SEQ (REF / ALT)	FLANK SEQ (REF / ALT)	REF. SEQ. ID	REF. POS	REF. ID	ALT	EXON	MUTATION TYPE	REVCODON	REF. CODON	ALT. CODON	CDNA SEQ. POS
Antihypertensive P (membrane bound)	XPINP2	AE10001	1	127	AGACATCTG CAG AGCATCATG	37	4023453	100	ALG2453	0	Start		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10002	4	525	AGACATCTG CAG AGCATCATG	38	4023453	101	ALG2453	0	Exon03		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10003	5	284	CTCCAGAGG CAG TCCTCCGAG	39	4023453	102	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10004	6	284	CTCCAGAGG CAG TCCTCCGAG	40	4023453	103	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10005	7	432	GGGCTTCTG CAG GAGTCTG	41	4023453	104	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10006	8	289	TATATATAG CAG GAGTCTG	42	4023453	105	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10007	10	481	TAATATAG CAG GAGTCTG	43	4023453	106	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10008	13	273	CACAGAGG CAG GAGTCTG	44	4023453	107	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10009	13	274	TTTCCAGG CAG TTTCCAGG	45	4023453	108	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10010	14	127	AGTCTCTG CAG AGCATCATG	46	4023453	109	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10011	15	184	CTCTCTG CAG AGCATCATG	47	4023453	110	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10012	15	184	CTCTCTG CAG AGCATCATG	48	4023453	111	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10013	15	211	TTTCCAGG CAG TTTCCAGG	49	4023453	112	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10014	16	221	TTTCCAGG CAG TTTCCAGG	50	4023453	113	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10015	16	138	ATATATAG CAG GAGTCTG	51	4023453	114	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10016	17	138	ATATATAG CAG GAGTCTG	52	4023453	115	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10017	22	800	GATATAG CAG GAGTCTG	53	4023453	116	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10018	22	800	GATATAG CAG GAGTCTG	54	4023453	117	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10019	25	195	TGATAG CAG GAGTCTG	55	4023453	118	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10020	27	405	GGTCTCTG CAG GAGTCTG	56	4023453	119	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10021	27	405	GGTCTCTG CAG GAGTCTG	57	4023453	120	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10022	28	710	TACATAG CAG TACATAG	58	4023453	121	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10023	28	1300	GATCTCTG CAG GAGTCTG	59	4023453	122	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10024	6	307	TGATAG CAG TACATAG	60	4023453	123	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10025	6	307	TGATAG CAG TACATAG	61	4023453	124	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (membrane bound)	XPINP2	AE10026	6	273	ATATAG CAG GAGTCTG	62	4023453	125	ALG2453	0	Non-CDS		CGG	CGG	1007241
Antihypertensive P (

[illegible]

GENE DESCRIPTION	LOCUS ID	NUM ID	CONTIG	MINI CONTIG POS	FLANK SEQ REF (REF/ALT)	FLANK SEQ ALT (SEQ ID NO.)	REF. SEQ. ID	REF. SEQ. POS	REF. ALT	EXON	MUTATION TYPE	REVCOMP	REF. COORD. ALT. COORD.	GENA. SEQ. ID	GENA. SEQ. POS
Brachyotin Receptor B2	BNRBR2	AE10427	4	1205	TGAAGGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.2	62978	G	A	Exon3	Non-CDS	1	NM_006231.1	3177
Brachyotin Receptor B2	BNRBR2	AE10428	4	2102	TGAAGGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.2	62979	T	A	Exon3	Non-CDS	1	NM_006231.1	3178
Brachyotin Receptor B2	BNRBR2	AE10429	4	2239	AGATGCTCTCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.2	62980	T	A	Exon3	Non-CDS	1	NM_006231.1	3179
Angiogenin Converting Enzyme 2	ACE2	AE10430	7	65	TGAAGAGATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869	48737	G	A	Intron12	Non-CDS	1	NM_006231.1	2254
Angiogenin Converting Enzyme 2	ACE2	AE10542	10	37	ATCATATATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869	48738	T	A	Intron12	Non-CDS	1	NM_006231.1	2255
Angiogenin Converting Enzyme 2	ACE2	AE10543	11	10	ATCATATATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869	48739	T	A	Intron12	Non-CDS	1	NM_006231.1	2256
Angiogenin Converting Enzyme 2	ACE2	AE10544	11	28	ATCATATATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869	48740	T	A	Intron12	Non-CDS	1	NM_006231.1	2257
Angiogenin Converting Enzyme 2	ACE2	AE10545	11	440	GAATGCTATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869.1	48842	G	T	Intron13	Non-CDS	1	NM_006231.1	50164
Angiogenin Converting Enzyme 2	ACE2	AE10546	11	109	GAATGCTATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869.1	48843	G	T	Intron13	Non-CDS	1	NM_006231.1	50165
Angiogenin Converting Enzyme 2	ACE2	AE10547	15	241	ATCATATATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869.1	48844	G	T	Intron13	Non-CDS	1	NM_006231.1	50166
Angiogenin Converting Enzyme 2	ACE2	AE10548	15	417	ATCATATATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869.1	48845	G	T	Intron13	Non-CDS	1	NM_006231.1	50167
Angiogenin Converting Enzyme 2	ACE2	AE10549	15	605	ATCATATATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AC035869.1	48846	G	T	Intron13	Non-CDS	1	NM_006231.1	50168
Protease Inhibitor 4	PI4	AE11084	3	166	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62653	T	G	Exon18	Non-CDS	1	AF211234.1	2173
Protease Inhibitor 4	PI4	AE11085	3	260	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62654	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11086	3	260	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62655	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11087	4	1685	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62656	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11088	4	1685	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62657	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11089	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62658	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11090	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62659	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11091	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62660	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11092	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62661	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11093	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62662	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11094	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62663	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11095	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62664	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11096	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62665	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11097	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62666	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11098	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62667	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11099	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62668	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11100	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62669	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11101	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62670	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11102	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62671	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11103	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62672	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11104	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62673	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11105	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62674	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11106	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62675	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11107	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62676	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11108	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62677	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11109	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62678	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11110	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62679	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11111	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62680	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11112	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62681	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11113	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62682	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11114	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62683	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11115	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62684	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11116	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62685	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11117	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62686	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11118	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62687	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11119	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62688	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11120	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62689	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11121	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62690	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11122	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62691	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11123	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62692	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11124	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62693	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11125	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62694	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11126	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62695	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11127	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62696	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11128	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62697	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11129	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62698	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11130	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62699	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11131	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62700	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11132	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62701	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11133	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62702	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11134	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62703	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11135	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62704	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11136	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62705	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11137	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62706	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11138	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62707	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11139	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62708	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11140	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62709	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11141	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62710	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11142	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62711	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11143	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62712	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11144	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62713	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11145	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62714	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11146	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62715	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11147	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62716	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11148	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62717	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11149	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62718	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11150	4	2020	GAATGACATCATTTAGGACAGA	ATATGGGAGGACATCATTTAGGACAGA	AL355102.1	62719	T	G	Exon18	Non-CDS	0	ATC	
Protease Inhibitor 4	PI4	AE11151	4	202											

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GENE DESCRIPTION	HGNC ID	SNP ID	CONTIG_NUM	CONTIG_POS	REF_AA	ALT_AA	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN (SEQ ID NO.)	FLANK_SEQ_REF (SEQ ID NO.)	FLANK_SEQ_ALT (SEQ ID NO.)	REFSEQ_FLANK_REF (SEQ ID NO.)
Antropodipidase P (membrane-bound)	XPNPE2	AE100a1	1	127	P	P	Exon20	Silent	0	CCC	CCG	AJB9694.1	607	4	37	100	163
Bradykinin Receptor B1	BDKRB1	AE103a1	6	307	R	Q	Exon2	Missense	0	CGG	CAG	NP_000701.1	317	8	80	123	186
Bradykinin Receptor B1	BDKRB1	AE103a2	4	273	P	P	Exon2	Silent	0	CCG	CCA	NP_000701.1	41	10	61	124	187
Tachykinin Receptor 1	TACR1	AE106a1	1	614	F	F	Exon1	Silent	1	TTT	TTC	NP_001049.1	111	16	81	144	207
Tachykinin Receptor 1	TACR1	AE106a2	2	789	I	I	Exon2	Silent	1	ATC	ATA	NP_001049.1	164	18	82	145	208
Tachykinin Receptor 1	TACR1	AE106a7	6	511	S	S	Exon5	Silent	1	TCG	TCA	NP_001049.1	378	20	87	150	213
C1 Esterase Inhibitor	C1NH	AE105a3	5	366	S	S	Exon7	Silent	0	AGC	AGT	NP_000553.1	406	24	90	153	216
C1 Esterase Inhibitor	C1NH	AE105a4	7	588	V	A	Exon3	Missense	0	GTT	GCT	NP_000553.1	58	26	91	154	217
C1 Esterase Inhibitor	C1NH	AE105a5	7	897	A	G	Exon3	Missense	0	GCA	GGA	NP_000553.1	159	28	92	155	218
C1 Esterase Inhibitor	C1NH	AE105a6	8	276	V	M	Exon8	Missense	0	GTG	ATG	NP_000553.1	480	30	93	156	219
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107a1	1	153	K	E	Exon4	Missense	0	AAA	GAA	NP_002248.1	186	34	94	157	220
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107a3	2	605	E	Q	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	38	96	159	222
Bradykinin Receptor B1	BDKRB1	AE103a6	1	67	N	N	Exon3	Silent	0	AAC	AAT	NP_000701.1	114	558	579	611	843
Bradykinin Receptor B1	BDKRB1	AE103a7	1	181	R	R	Exon3	Silent	0	AGG	AGA	NP_000701.1	152	553	590	612	844
Bradykinin Receptor B1	BDKRB1	AE103a8	1	286	L	V	Exon3	Missense	0	CTG	GTG	NP_000701.1	191	550	531	613	845
Bradykinin Receptor B1	BDKRB1	AE103a9	2	136	E	E	Exon3	Silent	0	GAG	GAA	NP_000701.1	233	582	582	614	846
Bradykinin Receptor B2	BDKRB2	AE104a19	7	339	R	C	Exon2	Missense	1	CGT	TGT	NP_000614.1	14	564	584	616	848
Bradykinin Receptor B2	BDKRB2	AE104a24	4	918	D	D	Exon3	Silent	1	GAT	GAC	NP_000614.1	311	568	599	621	853
Bradykinin Receptor B2	BDKRB2	AE104a25	4	1046	G	E	Exon3	Missense	1	GCG	GAG	NP_000614.1	354	569	590	622	854
Angiotensin Converting Enzyme 2	ACE2	AE109a7	15	241	N	N	Exon18	Silent	1	AAT	AAC	AF78220.1	690	843	601	633	665
Protease Inhibitor 4	P14	AE110a2	2	528	F	F	Exon2	Silent	0	TTC	TTT	NP_006208.1	233	574	603	635	667
Protease Inhibitor 4	P14	AE110a5	4	563	S	S	Exon1	Silent	0	AGT	AGC	NP_006208.1	189	576	606	638	670

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39

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37

Table VIIA

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
Coriell 24 panel	NA14905	African American	X	X	X	X	X			
Coriell 24 panel	NA14922	African American	X	X	X	X	X			
Coriell 24 panel	NA14923	African American	X	X	X	X	X			
Coriell 24 panel	NA14924	African American	X	X	X	X	X			
Coriell 24 panel	NA14925	African American	X	X	X	X	X			
Coriell 24 panel	NA14932	African American	X	X	X	X	X			
Coriell 24 panel	NA14933	African American	X	X	X	X	X			
Coriell 24 panel	NA14934	African American	X	X	X	X	X			
Coriell 24 panel	NA 17201	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17202	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17203	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17204	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17205	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17206	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17207	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17208	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA00576	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA03433	Chinese	X	X	X	X	X			
Coriell 24 panel	NA06090	Chinese	X	X	X	X	X			
Coriell 24 panel	NA07426	Chinese	X	X	X	X	X			
Coriell 24 panel	NA02345b	Japanese	X	X	X	X	X			
Coriell 24 panel	NA11589	Japanese	X	X	X	X	X			
Coriell 24 panel	NA14819	Japanese	X	X	X	X	X			
Coriell 24 panel	NA04535	Japanese	X	X	X	X	X			
Coriell 8 panel	NA14672	African American								
Coriell 8 panel	NA14682	African American								
Coriell 8 panel	NA14683	African American								
Coriell 8 panel	NA14696	African American								
Coriell 8 panel	NA14698	African American								
Coriell 8 panel	NA14700	African American								
Coriell 8 panel	NA14704	African American								
HD 50 AA panel	NA1850	African American								
HD 50 AA panel	3382	African American								
HD 50 AA panel	3725	African American								
HD 50 AA panel	6865	African American								
HD 50 AA panel	7754	African American								
HD 50 AA panel	10251	African American								
HD 50 AA panel	10378	African American								
HD 50 AA panel	12931	African American								
HD 50 AA panel	13294	African American								
HD 50 AA panel	14439	African American								
HD 50 AA panel	14441	African American								
HD 50 AA panel	14454	African American								
HD 50 AA panel	14464	African American								

Table VII B

DNA panel	Coriell Catalog #	Sample Description	XPBPEP2	BKRB1	BKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 50 AA panel	14537	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14583	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14681	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14687	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14697	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14699	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14720	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14746	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14754	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14755	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14771	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14772	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14783	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14826	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14837	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14862	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14863	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14864	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14892	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14893	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14894	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14895	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14897	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14900	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14901	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14903	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14904	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14905	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14922	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14923	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14924	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14925	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14932	African American	X	X	X	X	X	X	X	X
HD 50 AA panel	14933	African American	X	X	X	X	X	X	X	X
HD 100 GAU panel	NA 17201	Caucasian								
HD 100 GAU panel	17202	Caucasian								
HD 100 GAU panel	17203	Caucasian								
HD 100 GAU panel	17204	Caucasian								
HD 100 GAU panel	17205	Caucasian								
HD 100 GAU panel	17206	Caucasian								
HD 100 GAU panel	17207	Caucasian								
HD 100 GAU panel	17208	Caucasian								
HD 100 GAU panel	17209	Caucasian								
HD 100 GAU panel	17210	Caucasian								

Table VIIC

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17211	Caucasian								
HD 100 CAU panel	17212	Caucasian								
HD 100 CAU panel	17213	Caucasian								
HD 100 CAU panel	17214	Caucasian								
HD 100 CAU panel	17215	Caucasian								
HD 100 CAU panel	17216	Caucasian								
HD 100 CAU panel	17217	Caucasian								
HD 100 CAU panel	17218	Caucasian								
HD 100 CAU panel	17219	Caucasian								
HD 100 CAU panel	17220	Caucasian								
HD 100 CAU panel	17221	Caucasian								
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HD 100 CAU panel	17227	Caucasian								
HD 100 CAU panel	17228	Caucasian								
HD 100 CAU panel	17229	Caucasian								
HD 100 CAU panel	17230	Caucasian								
HD 100 CAU panel	17231	Caucasian								
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HD 100 CAU panel	17240	Caucasian								
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HD 100 CAU panel	17242	Caucasian								
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HD 100 CAU panel	17248	Caucasian								
HD 100 CAU panel	17249	Caucasian								
HD 100 CAU panel	17250	Caucasian								
HD 100 CAU panel	17251	Caucasian								
HD 100 CAU panel	17252	Caucasian								
HD 100 CAU panel	17253	Caucasian								
HD 100 CAU panel	17254	Caucasian								

ACE2

X **X** **X** **X** **X**

Omapatrilat Trial Samples 12 angioedema patients

GENE DESCRIPTION	HGNC ID	SNP ID	EXON	REVCOMP	PCR Amplicon Name	Target Name	PCR Left primer (SEQ ID NO.)	PCR Right primer (SEQ ID NO.)	PCR Right primer (SEQ ID NO.)
Annopeptidase P (membrane-bound)	XPNPE2	AE10051	Exon20	0	AE10097078	XPNPE2_X20a	AGTGTCTCTTCCTTCCTTC	TATTCAGTACCTGGGGTTGGG	380
	XPNPE2	AE10052	Intron3	0	AE1009810	XPNPE2_X3a	CAGCCCGAGCGCTTAATCTGA	CTCTACTTCCTCCCTTTGG	381
	XPNPE2	AE10053	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	382
Annopeptidase P (membrane-bound)	XPNPE2	AE10054	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	383
	XPNPE2	AE10055	Intron1	0	AE1009102	XPNPE2_X1a	TGATGTGACGAGCTGTTGTG	ACAGAAAAAGAGACTGGCG	384
	XPNPE2	AE10056	Intron7	0	AE10092528	XPNPE2_X7a	CAGGCTGGGCATACATG	GGCCCTGAATCTGCTATT	385
Annopeptidase P (membrane-bound)	XPNPE2	AE10057	Intron7	0	AE10092528	XPNPE2_X7a	CAGGCTGGGCATACATG	GGCCCTGAATCTGCTATT	386
	XPNPE2	AE10058	Intron10	0	AE10093768	XPNPE2_X10a	CTTCCTTTGAGCTCCAGAAC	CTGTCTCTCTCTGGGCTCT	387
	XPNPE2	AE10059	Intron10	0	AE10093768	XPNPE2_X10a	CTTCCTTTGAGCTCCAGAAC	CTGTCTCTCTCTGGGCTCT	388
Annopeptidase P (membrane-bound)	XPNPE2	AE10060	Intron10	0	AE10093768	XPNPE2_X10a	CTTCCTTTGAGCTCCAGAAC	CTGTCTCTCTCTGGGCTCT	389
	XPNPE2	AE10061	Intron13	0	AE10092528	XPNPE2_X13a	TAATGACACGCTCAGGGCTTG	GAGCTCTCAGGCTTTTCATT	390
	XPNPE2	AE10062	Intron13	0	AE10094950	XPNPE2_X13a	TAATGACACGCTCAGGGCTTG	GAGCTCTCAGGCTTTTCATT	391
Annopeptidase P (membrane-bound)	XPNPE2	AE10063	Intron13	0	AE10094950	XPNPE2_X13a	TAATGACACGCTCAGGGCTTG	GAGCTCTCAGGCTTTTCATT	392
	XPNPE2	AE10064	Intron13	0	AE10094950	XPNPE2_X13a	TAATGACACGCTCAGGGCTTG	GAGCTCTCAGGCTTTTCATT	393
	XPNPE2	AE10065	Exon1	0	AE1009102	XPNPE2_X1a	TGATGTGACGAGCTGTTGTG	ACAGAAAAAGAGACTGGCG	394
Annopeptidase P (membrane-bound)	XPNPE2	AE10066	Exon1	0	AE1009102	XPNPE2_X1a	TGATGTGACGAGCTGTTGTG	ACAGAAAAAGAGACTGGCG	395
	XPNPE2	AE10067	Intron8	0	AE10092930	XPNPE2_X8a	GGCCGCTATCTTAATGAGTAC	CTGCTGGCACTTTGTCTCT	396
	XPNPE2	AE10068	Intron8	0	AE10092930	XPNPE2_X8a	GGCCGCTATCTTAATGAGTAC	CTGCTGGCACTTTGTCTCT	397
Annopeptidase P (membrane-bound)	XPNPE2	AE10069	Intron17	0	AE10093568	XPNPE2_X17a	CCCTCTCTTAGCACACATC	CTGCTGGCACTTTGTCTCT	398
	XPNPE2	AE10070	Intron17	0	AE10093568	XPNPE2_X17a	CCCTCTCTTAGCACACATC	CTGCTGGCACTTTGTCTCT	399
	XPNPE2	AE10071	Intron17	0	AE10093568	XPNPE2_X17a	CCCTCTCTTAGCACACATC	CTGCTGGCACTTTGTCTCT	400
Annopeptidase P (membrane-bound)	XPNPE2	AE10072	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	401
	XPNPE2	AE10073	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	402
	XPNPE2	AE10074	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	403
Annopeptidase P (membrane-bound)	XPNPE2	AE10075	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	404
	XPNPE2	AE10076	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	405
	XPNPE2	AE10077	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	406
Annopeptidase P (membrane-bound)	XPNPE2	AE10078	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	407
	XPNPE2	AE10079	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	408
	XPNPE2	AE10080	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	409
Annopeptidase P (membrane-bound)	XPNPE2	AE10081	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	410
	XPNPE2	AE10082	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	411
	XPNPE2	AE10083	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	412
Annopeptidase P (membrane-bound)	XPNPE2	AE10084	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	413
	XPNPE2	AE10085	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	414
	XPNPE2	AE10086	Intron15	0	AE10095768	XPNPE2_X15a	TAGCTGTCTCTCTCTCTGGC	ATAGATGAGGCTCAGCTTGG	415
Annopeptidase P (membrane-bound)	XPNPE2								

GENE DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	PCR Amplicon Name	Target Name	PCR Left primer		PCR Right primer		PCR Right primer (SEQ ID NO:)
							PCR Left primer (SEQ ID NO:)	PCR Right primer			
Bradykinin Receptor B1	BKBRB1	AE10368	Exon3	0	AE10369p10	U48231_X2.12a	GCCTCTGATCTGGGTGTTTGTCT	CTGTGGTCTTGGTATCATCTTGG	707	739	
	BKBRB1	AE10367	Exon3	0	AE10369p10	U48231_X2.12a	GCCTCTGATCTGGGTGTTTGTCT	CTGTGGTCTTGGTATCATCTTGG	708	740	
	BKBRB1	AE10366	Exon3	0	AE10369p10	U48231_X2.12a	GCCTCTGATCTGGGTGTTTGTCT	CTGTGGTCTTGGTATCATCTTGG	709	741	
	BKBRB1	AE10365	Exon3	0	AE10369p10	U48231_X2.12a	GCCTCTGATCTGGGTGTTTGTCT	CTGTGGTCTTGGTATCATCTTGG	710	742	
	BKBRB2	AE104518	Exon1 or Exon2	1	AE104565p66	BKBRB2_X3.5a	GCCTTTGCCAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	711	743	
	BKBRB2	AE104518	Exon2	1	AE104565p66	BKBRB2_X3.5a	GCCTTTGCCAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	712	744	
	BKBRB2	AE104518	5'Flank	1	AE104565p90	BKBRB2_X3.5a	GCCTTTGCCAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	713	745	
	BKBRB2	AE104521	5'Flank	1	AE104565p90	BKBRB2_X3.5a	GCCTTTGCCAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	714	746	
	BKBRB2	AE104522	5'Flank	1	AE104565p88	BKBRB2_X1.1a	CTGTGGGATTTCTTTGATAGCCA	AGAGCCTACAGCAGATTCACA	715	747	
	BKBRB2	AE104523	5'Flank	1	AE104565p82	BKBRB2_X1.1a	CTGTGGGATTTCTTTGATAGCCA	AGAGCCTACAGCAGATTCACA	716	748	
Bradykinin Receptor B2	BKBRB2	AE104524	5'Flank	1	AE104565p68	BKBRB2_X1.1a	AGCAGACAGAGGAACCTCTCT	GAGGACGTTTTCGGCTCT	717	749	
	BKBRB2	AE104525	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	718	750	
	BKBRB2	AE104526	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	719	751	
	BKBRB2	AE104527	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	720	752	
	BKBRB2	AE104528	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	721	753	
	BKBRB2	AE104529	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	722	754	
	BKBRB2	AE104530	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	723	755	
	BKBRB2	AE104531	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	724	756	
	BKBRB2	AE104532	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	725	757	
	BKBRB2	AE104533	Exon3	1	AE104565p68	BKBRB2_X3.5a	GCAGCGGACAGGAATTAGTGCT	AGATCAGACAGAGAGAGAGGG	726	758	
Angiotensin Converting Enzyme 2	ACE2	AE10694	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	727	760	
	ACE2	AE10695	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	728	761	
	ACE2	AE10696	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	729	762	
	ACE2	AE10697	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	730	763	
	ACE2	AE10698	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	731	764	
	ACE2	AE10699	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	732	765	
	ACE2	AE10700	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	733	766	
	ACE2	AE10701	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	734	767	
	ACE2	AE10702	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	735	768	
	ACE2	AE10703	Exon1	0	AE10695p30	ACE2_X13a	CACCATACGAGAGAAAGAACCA	GGAGTCTGCTGCTGCTGCTGCTGCT	736	769	
Protease Inhibitor 4	P4	AE11068	5'Flank	0	AE11069p56	P4_X1.12a	ATGGTGAGACACCGGACGCTAT	TGTACCGCTATACAGACAGAG	737	770	
	P4	AE11069	5'Flank	0	AE11069p56	P4_X1.12a	ATGGTGAGACACCGGACGCTAT	TGTACCGCTATACAGACAGAG	738	771	
	P4	AE11070	5'Flank	0	AE11069p56	P4_X1.12a	ATGGTGAGACACCGGACGCTAT	TGTACCGCTATACAGACAGAG	739	772	
	P4	AE11071	5'Flank	0	AE11069p56	P4_X1.12a	ATGGTGAGACACCGGACGCTAT</				

Table IX (1 of 2)

[illegible]

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNIPIT	ORCHID_SNIPIT (SEQ ID NO:)
AE100s1	TATCATTTTGTGCTATGACCG	1066	CAGGTCAGGAGAGAGGC	1154	CCTCATGATGTCGCGCTGTCTCC	1242
AE100s10	AAACTTATCATCATGAGGTACAAAG	1067	GAGGACATTTTATTCACATCTCTC	1155	GTGGTTTGAACCTTACGATGCAC	1243
AE100s11	ATAGAATGATCTCTCCAGAGGGA	1068	CAGCTTAACCTGTACTGGG	1156	TGGAAGCCCGAGNCCCGAGAGGT	1244
AE100s12	TCCAGAGGACTGGCGCTG	1069	GAAGGAGCGCTTAACCCCTG	1157	AGCCAGGCGCCAGAGGTCTCCCA	1245
AE100s13	ATAGATGACTTCTCCAGAGGGA	1070	GCTGAGAAGGAGGAGATGTT	1158	AATGTTGAGAANGAGCCTAACCTG	1246
AE100s14	N/A	N/A	N/A	N/A	N/A	N/A
AE100s15	ACCTCTGTCTGCTCGAG	1071	GATGAGGAGCAAGGAG	1159	CCGGGCTCTCTTCANGCINTTCT	1247
AE100s16	AAAGAGGAAGGAAGAAAGGAA	1072	GTGTAGATPAGAGAGGGTTATAGG	1160	AGAAAAGCTGCTCAGCAGATCAGC	1248
AE100s17	N/A	N/A	N/A	N/A	N/A	N/A
AE100s18	AACACAGACAGACCCCTCTCA	1073	GATCCAGAGATCTCTATGAC	1161	TACCTTAATAATAATAAAGCCAG	1249
AE100s19	N/A	N/A	N/A	N/A	N/A	N/A
AE100s2	ATAGAAATTTGAGGGCAGGG	1074	GTATCTTTGAGGTTCACTCC	1162	GCAACAGTCTCTTTTNCAGAACAGTC	1250
AE100s20	TACCACACAGGGACTGG	1075	GATTCAGTACTGAGCTGG	1163	AGACTTCACCTCTTGCACTTGGCTT	1251
AE100s21	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGTCTAAGGACACACAAATTT	1076	GAGTGGGCTCAGGGACT	1164	CTGCATGTTGCTGAAGGTTGAAAGA	1252
AE100s24	CGCTATCTGATCTCATCATCT	1077	CGCACCTGGAGTGGGG	1165	TTTNGAGCCTGTGCTNCACACAGACT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAAGTAAGGTTTGTGAGAAAGG	1078	GAGCCCCAAAAGTGAAGTGA	1166	TTACCTTANGGCTGACCTNCCAGGAAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A	N/A	N/A
AE100s30	TATCTTTTCTTACAGTTGGCACCA	1079	CAATGACAGAGGAAGGG	1167	TCACCTGGCTCTCACCGAGATTC	1255
AE100s4	TCCCTGTGCTCTCCCGG	1080	AATATTTGTCAGTATTTACAGATAG	1168	TATTTGNCACACTGACANGGCTGAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGTCATGAGGTAGGTG	1081	CTTTGTCTTTTCCACTCTGTGAAA	1169	ACCTTCATGAGGGTATATAAAG	1257
AE100s7	ATCCAGTAAATGCAAGCCAG	1082	GTCCAGCTTAGGGTAAACGTTTG	1170	AAGAGTTTCTTTTGAAGAAAGGTTT	1258
AE100s8	GCAAAATCTACGTCGTCTG	1083	CAGGTCGTGGGGGACAGTA	1171	GTAAGAGGCTCTCNATNGACACAGGG	1259
AE100s9	AAAACTAGGAAGACAGAAAGCACAC	1084	TTTTCAGAGGACTGGCAGAG	1172	CACAGAGTAGAGAGNATTTGCCACGAAA	1260
AE103s1	AACTTCTTTGCTTCACTAACGCT	1085	GATGAGATATTTGGAGCAAGACTTTTAG	1173	CCAGTAAATTTATGCTTTTGTGGGCC	1261
AE103s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGAATGTTACCAATTT	1086	GACTGTGACCTCTCTGCTC	1174	ATCCTGAAATTTCCAAAGTGGGCCCT	1262
AE103s12	N/A	N/A	N/A	N/A	N/A	N/A
AE103s13	CCACGAGTTTCTGTGTAATTTG	1087	CTTTGAATAGCAATGGAAGTGTARTAGA	1175	CAGCAGGAACAATAAACAAGTATC	1263
AE103s14	TGTATAGCAGCAGCAGGAA	1088	CCTGGCAGTTAGCTTAGAAGC	1176	ACAAGTATCGGTATATGNCCTCTTA	1264
AE103s2	TGCAATGCTCCAGAGGCC	1089	CAACAGGACAAAGAGTTCC	1177	CTGGGACCTGCTGNACAGAGTGTGCC	1265
AE103s3	ACTTTTCTGGCGGAATTAACA	1090	ACCCGCCAATCTAGGGA	1178	TGAACCAANANGCTTGGCTTCTTATC	1266
AE103s4	N/A	N/A	N/A	N/A	N/A	N/A
AE103s5	N/A	N/A	N/A	N/A	N/A	N/A
AE103s6	TTCTGGCAGAGAAATATCTGA	1091	CCACAGGAGATGCTGATG	1179	GAGCCTCTCTGCGCTGTCATCAA	1267
AE103s7	N/A	N/A	N/A	N/A	N/A	N/A
AE103s8	ATCTGACATCACCGCT	1092	GTAGTTGAGAGAGCAGATCGC	1180	AGATCTGAACATCACCGCTGATC	1268
AE103s9	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1	GAGACAAATATCTGTTTTTGATAA	1093	CTCACCTGCTGCTTGTG	1181	CACCTGGGCAATGNGGNGGCTCCGCC	1269
AE104s10	GGTTGGGGGCTCAGGGTG	1094	GTGGCGGTGTGAAGCAC	1182	GTNGGATGACAGGTNGAAGGAGGCA	1270

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:1)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:1)	ORCHID_SNPLIT (SEQ ID NO:1)	ORCHID_SNPLIT (SEQ ID NO:1)
AE104s11	TTGGATCTGAATGCTTCTTG	1095	GCCCTATGCTGATGATG	1183	TTACACATATAACGNCATCTGAGTCTT	1271
AE104s12	ATTTCTCGTTGGATGTGAATG	1096	CGGCCCTATGCTGATGATG	1184	TAACAGCTCATTTGAGTCTTTKACAG	1272
AE104s13	GCCATTTGGCGCAGCTC	1097	AAAAAGAGGCTGTGTTTTGCA	1185	GGGCGCTCATCTCAGCACACAGACAC	1273
AE104s14	AAGTGAATGATGCTGCCCT	1098	AAGGTGCCCGATGATGAGC	1186	CCCTAGAAGAGTGTGAAGAAAGATG	1274
AE104s16	GATGCAATGATGAGGAGG	1099	CATGATGGGATTCATTATCC	1187	ATTCTTTCATCTCATNTATNTAAACAAA	1275
AE104s17	GATGCAATGATGAGGAGG	1100	CATPAATGCCCTCCTCCAT	1188	TACGTTGAGCGATGATGCCCAAGT	1276
AE104s18	AGAAGAAAGATGTTAGATGCA	1101	CATTGAGTCAGGACTCAGCA	1189	ACAGGGCTGGGATNGCCCATATAC	1277
AE104s19	TAACTAGTGAATCAGGAATCCCTTT	1102	CACCTGAGTCAAAATGTTCTTC	1190	GTGCTGGCGCGGATGCTCTCAC	1278
AE104s2	GAGACAATAATCTGTTTTTTGATAA	1103	CTCACCCTGCTGCTGTTG	1191	GTGAGGAGGGGNCACCTGGGCGGG	1279
AE104s20	TTTACACATCCAGGCGCTGAG	1104	CTCTTCCCGACATCACTGG	1192	TTTTTGNAGCTTAAACACCTTCTTTC	1280
AE104s21	GGATTTCTTTGTATGCCACGTAC	1105	CATPACATCTCGAAGAACGG	1193	GCAGAAGCTGCTCTGTTTCTCTGGT	1281
AE104s22	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGAGTGCGGCGG	1106	GCAGAGTGGAGAGCTCAG	1194	GAAGTGGCCAGGAGGCTGNTGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A	N/A
AE104s26	TGAATAGATTAAAGAAACCCAGG	1107	GTTCCTCCCTCCCTGCCCC	1195	CATTGCACCAAACTGGATGGC	1283
AE104s27	TCGACCCCTCTGTCGGAAC	1108	GAAAGAGAGGAGCCATCTCA	1196	GCTTTGNGTGTGNCAGTGGCCAGTC	1284
AE104s28	N/A	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A	N/A
AE104s3	TTTGAAGGAGGAGATC	1109	CAACCTCACTCCAGC	1197	GAGCGAAGGGCTGGCTGAGGTGATG	1285
AE104s30	N/A	N/A	N/A	N/A	N/A	N/A
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGATACATGCTAGGAGCT	1110	GTTTGGACCCCAAGTTCTAT	1198	ACCTTTTGTGTTGATTTTTCAGTGA	1286
AE104s34	ACATGCTGCTTCACACG	1111	GTACATGTGAGGCACTWTACGC	1199	GGTCCCAATAGTATGCTGCTCA	1287
AE104s35	N/A	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTCTCTGCTCCATATCA	1112	CATCTGAAGGAACCTCAAGACTCA	1200	ACCACAGCACCTGCTGACCGTCTC	1288
AE104s4	AGTGAGAGCTTTGAGTGCA	1113	CTTTGATGATAAAGAGGAGCA	1201	AGGTTCCAGGAGAGCTGGATGAGG	1289
AE104s5	TGCAGGCTTCAGGAGAGA	1114	CAAGAGAGGCGTCTTTGGAT	1202	GCTGGGATGANGYCTGGGTGCTGCT	1290
AE104s6	GGCTCAACACTGTGGAATGTC	1115	CAAGAGGCGCTGCCCGA	1203	GTCTCTGGAGAAAACACTGTGCTG	1291
AE104s7	AACTGTGGCCACAGAGGT	1116	AACTCTTACCCACACG	1204	CCCTCTCCCAAGCTGTTGCTCCACAA	1292
AE104s8	ATGTAGTAGCACCTTTTGTCTT	1117	GBAGACCAAGTTCTCAGCTC	1205	GAAGAGGAACTGAGCGCGGAGCAG	1293
AE104s9	TATTTCTAGACTCAGTGTCTTTTCTTTATAG	1118	GAAGTCTGTGAGGTTTAAAG	1206	AAGGCTGCTACGTANATNTAGGATC	1294
AE105s1	GAGAGGACTCTGAGGGGG	1119	AGGCTTCACTGCTCTGCA	1207	CCAGCGCTGGGGAAGAAAGAGACA	1295
AE105s2	ATTGTGACAGAGGTGGGG	1120	CAACTCAGATTTGGGAGGC	1208	GAGATGCGGTAGGAAGACTGTTAAG	1296
AE105s3	N/A	N/A	N/A	N/A	N/A	N/A
AE105s4	GCGAAGGAGGTTGCGAA	1121	TTGAGTTGGTTGTCGCA	1209	AAGCTGGAANCCCTNAGGATGGTTCA	1297
AE105s5	TGTTGGGGATGCTTTGG	1122	GATGCTGAATGGGGAAGG	1210	AAGCTTACACGCTTCTCAG	1298
AE105s6	ATCTCTGTGGCCGAC	1123	CATPACTGCCCCATGAGAC	1211	GGACTTGTNCTNCTGTTCCAGAGCA	1299
AE106s1	TATCAAGGCGCACGCG	1124	CACACGAATGGTACTACGC	1212	TACTGGCGAAGACAGCGCGATGGG	1300
AE106s2	ATGCTCTGTGTTGAGTAGTACG	1125	CATCATACATCCCTCCAGC	1213	CCAGGAGGAGAGCCAGGACCA	1301
AE106s3	ATPACTGGGATATTTTGTG	1126	CTACCGAGCGAAGTCTG	1214	CCAGGCGAGGTGAGGAGCGG	1302
AE106s4	TGCGAATATCATCTGAAATGA	1127	CTGTGTGACTCAACCAATCACT	1215	AGTCTGGACCACTTTTCCCAA	1303
AE106s5	AAAAGCTGCTCGACCTTTTAT	1128	TCAAAAATCTCAATCTTCTCCCTATCT	1216	TCCCTATCTTTTGCNACNCTNATGCTGT	1304
AE106s6	TTTGTAGTCAACAGCATGAGG	1129	CATGGAATTCCTCTCATCTG	1217	ACCCATPACTGACCTTTTGTGCAAGTCC	1305
AE106s7	ATGCTCTTGGAGTCACTTCGTG	1130	CCCACGAGGAGGACCCAG	1218	AGAGCAGTTNGAGTGCAGGTCNACGGGA	1306

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO.)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO.)	ORCHID_SNIPIT	ORCHID_SNIPIT (SEQ ID NO.)
AE1068	N/A	N/A	N/A	N/A	N/A	N/A
AE1069	N/A	N/A	N/A	N/A	N/A	N/A
AE1070	GTTCGTAGTCTCATTTCCAGATGATC	1131	ACACACAGCATGAATCTGTGCAC	1219	CABAACTCTGCTATATGATGATGC	1307
AE1071	AGCATCGAACACAGAGAAATTTATG	1132	CTTCCTCGCCCTTTCTC	1220	TCCCTTGNACRCAGGATCCCATCCC	1308
AE1072	CTGTGATACCATCATCAGATG	1133	CATCAATTTCTCTGTTCTGATGC	1221	GCTGTAGTTCGNGAGTTGCCACC	1309
AE1073	ATCGAACCCAGAGAAATTTGATGG	1134	GGGAGAAAAGGGCTGCA	1222	AAGGCRGGATGGGACTCTTG	1310
AE1074	ACCTGGACCACTCGGCT	1135	CTTTCCCCCACTGCTGG	1223	TGNGGCCACCCAGCTGTGTCA	1311
AE1075	CCAGTAAATCAATGTGATCC	1136	CAGCCTCAGCCGAGTGG	1224	ATGTGTGTCACTTTCTGCCATCACC	1312
AE1076	AATAGCTTATCCATAGGATAGGTTACTTT	1137	GAATGATTAATTTTGTGTCACAGTC	1225	ATCTGGAACTTATAGTNTTGAAGA	1313
AE1077	GGGGTTTCAGGGCCCTTTT	1138	GCAAAATTTAGCCAAAGTCAAGAGA	1226	GAGGGTTTCCAGANGTACNTATATTTA	1314
AE1078	TGGGGCCAAAGGAGCTAG	1139	GCTGAAAGACCAAGCAAGATTC	1227	AAGTGAACAAGGAATGGGTGTGAAA	1315
AE1079	GTGTTGAAACACACATATCTGCAAT	1140	TGGAAAGTTTCTAACCCAGATAATC	1228	TCATAATCAGNANTNAAANTTAGTAGC	1316
AE1080	GTGTTCACTGCAAAATTAAGATAATAACA	1141	ACATGGCAAGAGATAAATTTGCTG	1229	GAATTTTCTGAGAGAAATGCTAA	1317
AE1081	AACCTCAAACTAAGATTTATCCCTG	1142	GTACCAAAATACAAACAATAACCACTATT	1230	CACATCTAAATGACTCAGATAATG	1318
AE1082	CCCTCACCTTTAGATGAAAGTAA	1143	TTTGAACCCAGATCTCTTTTAAATTT	1231	TTCAAGTTCTAGGAATNATATCAGACAC	1319
AE1083	N/A	N/A	N/A	N/A	N/A	N/A
AE1084	AGGCTCACTCAAAAGGCAAT	1144	TGCTCTCTGCTCATTTG	1232	CTTGTTAANAAGCCCATNAAATCTTC	1320
AE1085	N/A	N/A	N/A	N/A	N/A	N/A
AE1086	CACCTTGACGTGGATGAG	1145	ATGTGGCATTTGGTCTGG	1233	GGNTGGACCGAGGNTGCGAGCCAC	1321
AE1087	CACCTCTGCACATCTCA	1146	CATGGTGTCTATTCAGGATTTTG	1234	AACCTCNCGGNCATGGCTGGAAACA	1322
AE1088	AGATTTGGGGGAGAACTGG	1147	CAGTAGAACTGGCTTTTATTTATGACC	1235	TNTCTTGGACAGATGTATNATATGAAA	1323
AE1089	CTGTACCTTTCTTTTCTATCTTCCCTT	1148	GCAGCATCATCGGCCACC	1236	CGGACTGNTGTGTTCTCATCAACATA	1324
AE1090	AAGGAGGGCTCTGCCAG	1149	GATGCAACTCTAGCTCTTTGTAATAAT	1237	GATCTGGCTTTGTTCTANTTCTAATG	1325
AE1091	N/A	N/A	N/A	N/A	N/A	N/A
AE1092	CTTATCAACGACACGTCAGAA	1150	GAATTAGCATATACCAATGATCTGACTCT	1238	GAGGGAAGATTTGTGATTTGGTCAG	1326
AE1093	GTCAAACTAAATGGCTGAAGTGG	1151	TTTCAGATGATTTGATTTCTATGATGC	1239	AGACCTTAAATTAACCTCTGAGGAT	1327
AE1094	AGGGTCAAACTAAATGGCTGAAA	1152	CATTTGCTTTTACATGATGATTTGTTTC	1240	TAAACCATATAAAGCACCTCCACAGA	1328
AE1095	AGAACTGGAGTATCTTTCTTGA	1153	CTGTAGAGGTGATGAAAGTGTCTTTG	1241	TATGAAAAGNGTACCAANTTCTATCCCC	1329
AE1096	N/A	N/A	N/A	N/A	N/A	N/A

SNP_ID	GBS_LEFT	GBS_LEFT (SEQ ID NO.1)	GBS_RIGHT	GBS_RIGHT (SEQ ID NO.1)
AE100s1	TGTTAAACGACGCGCGATGATGTTCTCTCTCCCTCACT	1330	CAGGAAACACGCTATGACACGAGAGCTCTGGGGTCTC	1451
AE100s10	TGTTAAACGACGCCGCTAGGCGATCTACACGATGATTCAGT	1331	CAGGAAACAGCTATGACACCCACACGCGAAGCAATC	1452
AE100s11	TGTTAAACGACGCCGCGATGTTCTGGGCTTTACCCCTCTCTC	1332	CAGGAAACACGCTATGACACGAGTCTGAGCAGAGACA	1453
AE100s12	TGTTAAACGACGCCGCGATGTTCTGGGCTTTACCCCTCTCTC	1333	CAGGAAACAGCTATGACACGAGTCTGAGCAGAGACA	1454
AE100s13	TGTTAAACGACGCCGCGATGCTAGTGCGAGATTTAACAGAC	1334	CAGGAAACAGCTATGACACGAGTCTGAGCAGAGACA	1455
AE100s14	TGTTAAACGACGCCGCGATGCTAGGATGATGTCACATCCG	1335	CAGGAAACAGCTATGACACCATGACATCAACACAGAG	1456
AE100s15	TGTTAAACGACGCCGCGCTCTCACACCCCTATCCTACAGG	1336	CAGGAAACAGCTATGACACCATGACATCAACACAGAG	1457
AE100s16	TGTTAAACGACGCCGCGCTACGATGAGATCTTGCACATGC	1337	CAGGAAACAGCTATGACACCCACATTAAGGAAAAGCC	1458
AE100s17	TGTTAAACGACGCCGCGCTACGAGCAGACAAATGATGATG	1338	CAGGAAACAGCTATGACCTGAGCTCTCTCTGAGATCT	1459
AE100s18	TGTTAAACGACGCCGCGCTATGACAGTATGCTGTGCATGT	1339	CAGGAAACAGCTATGACCATACGATGCTATCTGTGGA	1460
AE100s19	TGTTAAACGACGCCGCGCTACAGAGGAAGCACGATGATG	1340	CAGGAAACAGCTATGACACACTGGTGTTCGTAACACC	1461
AE100s2	TGTTAAACGACGCCGCGCTTGTAAAGCCCTTTCGACAGAT	1341	CAGGAAACAGCTATGACCTGTGTAGTCAACAAGCC	1462
AE100s20	TGTTAAACGACGCCGCGCTCTGAAAGCCCGCCACAGAGAT	1342	CAGGAAACAGCTATGACCTCTGTTGAGAGCCTCTGGA	1463
AE100s21	TGTTAAACGACGCCGCGCTACGAGGCTCTCAGACCTCTCTGTT	1343	CAGGAAACAGCTATGACCGGAGAGCTCTGATAGCAGT	1464
AE100s22	TGTTAAACGACGCCGCGCTATGCTCTAGAAACCTTTTGA	1344	CAGGAAACAGCTATGACCTCTCTCTCTCTCTGGGGTTT	1465
AE100s23	TGTTAAACGACGCCGCGCTAGTACGACACGATCAATGCTGTT	1345	CAGGAAACAGCTATGACACCACTTGTGTCGACGATCT	1466
AE100s24	TGTTAAACGACGCCGCGCTAGCGCTACGACACAGAGACTCT	1346	CAGGAAACAGCTATGACACGAGTCTGTGTCGACGATCT	1467
AE100s25	TGTTAAACGACGCCGCGCTAGGAGCAAGTCTCTCTCCGCG	1347	CAGGAAACAGCTATGACCCCACTGTGAACTCTGTGAG	1468
AE100s26	TGTTAAACGACGCCGCGCTATGCTCTGCTCTGTACTTTTC	1348	CAGGAAACAGCTATGACCGGACACTCTCTCTACTTCCA	1469
AE100s27	TGTTAAACGACGCCGCGCTATGCTCTGCTCTGTACTTTTC	1349	CAGGAAACAGCTATGACCGCTCTGCAAACTCCACACT	1470
AE100s28	TGTTAAACGACGCCGCGCTGGGTGTATATCAACACCCCTGG	1350	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTATG	1471
AE100s29	TGTTAAACGACGCCGCGCTGAGATATGAGAAGCCAGCTTAG	1351	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTGTT	1472
AE100s3	TGTTAAACGACGCCGCGCTACTTGTGGAAGACACACAGA	1352	CAGGAAACAGCTATGACCTCTGCTGAGTGGGCTGTAAT	1473
AE100s30	TGTTAAACGACGCCGCGCTAGAGAAATTTGAGGCCATCACT	1353	CAGGAAACAGCTATGACCCCTCTCTCTCTCTCTCTCTG	1474
AE100s4	TGTTAAACGACGCCGCGCTAGAGTCAAGATCCCTCTTCCAT	1354	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1475
AE100s5	TGTTAAACGACGCCGCGCTAGGAAGCTCTCTCTCTCTCT	1355	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1476
AE100s6	TGTTAAACGACGCCGCGCTCAAGTGTGACAGTCTTCTCGTGA	1356	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1477
AE100s7	TGTTAAACGACGCCGCGCTCTCTATAGCAGCCCTATTGA	1357	CAGGAAACAGCTATGACCGGACCGCAGATACTTTTC	1478
AE100s8	TGTTAAACGACGCCGCGCTATCCGAGACAGGAGGTTTCAT	1358	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1479
AE100s9	TGTTAAACGACGCCGCGCTATCCAGAGACAGGAGCTGAT	1359	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1480
AE103s1	TGTTAAACGACGCCGCGCTTTTGGCTTCTCTCTGGAATTC	1360	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1481
AE103s10	TGTTAAACGACGCCGCGCTCTCCAGATCTGAAATATAC	1361	CAGGAAACAGCTATGACCGACCTCTCTCTCTCTCTCT	1482
AE103s11	TGTTAAACGACGCCGCGCTGAACACAGAGCTCTGAGCTTC	1362	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1483
AE103s12	TGTTAAACGACGCCGCGCTATCCAGATCTCAAGGAT	1363	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1484
AE103s13	TGTTAAACGACGCCGCGCTCAAGTATCTCTCACTTTGGT	1364	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1485
AE103s14	TGTTAAACGACGCCGCGCTCTCCACTTTGGTCTCCCATPA	1365	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1486
AE103s2	TGTTAAACGACGCCGCGCTGTAGTCTGCTCTCTCTCTCT	1366	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1487
AE103s3	TGTTAAACGACGCCGCGCTCTGAGCTCTCTCTCTCTCTCT	1367	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1488
AE103s4	TGTTAAACGACGCCGCGCTCTGGAACACAGACACTTTAA	1368	CAGGAAACAGCTATGACCAAGGAGAGATGAGATCTAGA	1489
AE103s5	TGTTAAACGACGCCGCGCTATCTCCAGATCTCAAGGAT	1369	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1490
AE103s6	TGTTAAACGACGCCGCGCTCTCTCTCTCTCTCTCTCTCT	1370	CAGGAAACAGCTATGACAGTCTGTGAGGAGAAACC	1491
AE103s7	TGTTAAACGACGCCGCGCTCTCTCTCTCTCTCTCTCTCT	1371	CAGGAAACAGCTATGACAGTCTGTGAGGAGAAACC	1492
AE103s8	TGTTAAACGACGCCGCGCTCTCTCTCTCTCTCTCTCTCT	1372	CAGGAAACAGCTATGACCTCTCTCTCTCTCTCTCTCT	1493
AE103s9	TGTTAAACGACGCCGCGCTCTCTCTCTCTCTCTCTCTCT	1373	CAGGAAACAGCTATGACAGATCTCTCTCTCTCTCTCT	1494
AE104s1	TGTTAAACGACGCCGCGCTCTCTCTCTCTCTCTCTCTCT	1374	CAGGAAACAGCTATGACGATCTCTCTCTCTCTCTCTCT	1495
AE104s10	TGTTAAACGACGCCGCGCTCTCTCTCTCTCTCTCTCTCT	1375	CAGGAAACAGCTATGACGATCTCTCTCTCTCTCTCTCT	1496

Table XI (2 of 3)

AE104s11	TGTAAAACGACGGCCAGTTCGGGAGTTGTAAACAATGCT	1376	CAGAAAACAGCTATGACGACGAGCTGTGTGTTGTCA	1497
AE104s12	TGTAAAACGACGGCCAGTGTCTATGCAAAAACCTCATCCA	1377	CAGAAAACAGCTATGACGACGAGCTGTGTGTTGTCA	1498
AE104s13	TGTAAAACGACGGCCAGTCTATACACCATCATAGGCGC	1378	CAGAAAACAGCTATGACCTGTGGAGGAAGAAAACAGG	1499
AE104s14	TGTAAAACGACGGCCAGTGTAGCTCTCCAGTGTCTAGCCC	1379	CAGAAAACAGCTATGACCTCATTTCTAAATCGGCTCTTG	1500
AE104s16	TGTAAAACGACGGCCAGTAAATAAAGAGGTGCTGACCCAC	1380	CAGAAAACAGCTATGACCTCTAGAAATCATAGCGCCA	1501
AE104s17	TGTAAAACGACGGCCAGTCCACCATGACCCCAAGTTTATP	1381	CAGAAAACAGCTATGACCGCCACCTGTGTTTCATACT	1502
AE104s18	TGTAAAACGACGGCCAGTGAGGAATCCCTTTGACTCACC	1382	CAGAAAACAGCTATGACGACTGAGCAATGTCTGTGG	1503
AE104s19	TGTAAAACGACGGCCAGTGTGTTCTTCAACTGTGTTGCC	1383	CAGAAAACAGCTATGACCAACAAAGCTCCATTTGAGT	1504
AE104s2	TGTAAAACGACGGCCAGTGTGTTTAAAGAGGCGCTG	1384	CAGAAAACAGCTATGACGACTTTTTCACCAACCG	1505
AE104s20	TGTAAAACGACGGCCAGTATATATGCGGAGGTTTCT	1385	CAGAAAACAGCTATGACCGCCACCCCAATAAAGTGT	1506
AE104s21	TGTAAAACGACGGCCAGTTTTTGGATGTAAACAGTGGGC	1386	CAGAAAACAGCTATGACCAATGTGTTTGAAGTCCC	1507
AE104s22	TGTAAAACGACGGCCAGTGGAGCCCAATGTGTAATAAT	1387	CAGAAAACAGCTATGACCTGTGAGCAAACTGTGAGA	1508
AE104s23	TGTAAAACGACGGCCAGTCTTCCAGTCGCTCCCTGGTAC	1388	CAGAAAACAGCTATGACCAACATGTGAAATCTTTCGA	1509
AE104s24	TGTAAAACGACGGCCAGTCTCCATCTGATATGGGTTCTG	1389	CAGAAAACAGCTATGACCAACGAGATGAGAAAGTTTC	1510
AE104s25	TGTAAAACGACGGCCAGTAAAGCACTGTCCCTCAATCCT	1390	CAGAAAACAGCTATGACCTTAATCATACAGATCGCC	1511
AE104s26	TGTAAAACGACGGCCAGTCACTCTCTTGTCCATCAGTGA	1391	CAGAAAACAGCTATGACCCCAAGGACTCCAAATATC	1512
AE104s27	TGTAAAACGACGGCCAGTCCCTCACAAGCACTTCATGTT	1392	CAGAAAACAGCTATGACCTCTACTGTATGGACAAGGA	1513
AE104s28	TGTAAAACGACGGCCAGTCTCTCAATATGCTCTCTGTG	1393	CAGAAAACAGCTATGACCGGGGTATATGGACAGCA	1514
AE104s29	TGTAAAACGACGGCCAGTGTCTCAGCACTGTGATCTCTC	1394	CAGAAAACAGCTATGACCGTGTACTGATCATGTGA	1515
AE104s3	TGTAAAACGACGGCCAGTCCCAATATCATGTCTGCTCCA	1395	CAGAAAACAGCTATGACCTGTGGATGAAAAGAGGGA	1516
AE104s31	TGTAAAACGACGGCCAGTGTGTTCTTCAACTGTGTGTC	1397	CAGAAAACAGCTATGACCGGAACTCAAGACTCAA	1517
AE104s32	TGTAAAACGACGGCCAGTCTGACTCAATGGACGTTTGT	1398	CAGAAAACAGCTATGACCTTGAGTCAGGGACTCAG	1518
AE104s33	TGTAAAACGACGGCCAGTCTCAATGGACGTTTGT	1399	CAGAAAACAGCTATGACCAATCCATATTTACACCA	1519
AE104s34	TGTAAAACGACGGCCAGTATCTTCTGCTGCTCATCACA	1400	CAGAAAACAGCTATGACCTATTTGACCAACCATCTG	1520
AE104s35	TGTAAAACGACGGCCAGTCTCAGACTTTGAAGACATGCCC	1401	CAGAAAACAGCTATGACCTCACTCATGTGGACAAGGA	1521
AE104s36	TGTAAAACGACGGCCAGTCTGTAAGTACACCTTTGCTT	1402	CAGAAAACAGCTATGACCAACATTTCCAGCAAGGA	1522
AE104s4	TGTAAAACGACGGCCAGTGAATCCCAAGAGATTGAGGC	1403	CAGAAAACAGCTATGACCAAGCTTTGGAGGAAGC	1523
AE104s5	TGTAAAACGACGGCCAGTGAATCCCAAGAGATTGAGGC	1404	CAGAAAACAGCTATGACCAACATTTCCACACTTTGTG	1524
AE104s6	TGTAAAACGACGGCCAGTGTCTCTTTTTCATCCAA	1405	CAGAAAACAGCTATGACCCAGCTTACAGGAAGTGG	1525
AE104s7	TGTAAAACGACGGCCAGTGGACCCCAAAATCAATGCTT	1406	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1526
AE104s8	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1407	CAGAAAACAGCTATGACCATACCAACAGCTTCCCC	1527
AE104s9	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1408	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1528
AE105s1	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1409	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1529
AE105s2	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1410	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1530
AE105s3	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1411	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1531
AE105s4	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1412	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1532
AE105s5	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1413	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1533
AE105s6	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1414	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1534
AE106s1	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1415	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1535
AE106s2	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1416	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1536
AE106s3	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1417	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1537
AE106s4	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1418	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1538
AE106s5	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1419	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1539
AE106s6	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1420	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1540
AE106s7	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1421	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1541
AE106s8	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1422	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1542
AE106s9	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1423	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1543
AE107s1	TGTAAAACGACGGCCAGTGTGGAAATGACAGGTGGAAG	1424	CAGAAAACAGCTATGACCCAAAGACTCAAGTGGGA	1544
				1545

AE107s2	TGTAAACGACGGCCAGTCTCTGACAGAGCGTCTGTATAC	1425	CAGGAAACAGCTATGACCATTTTGGAGGTCCACACA	1546
AE107s3	TGTAAACGACGGCCAGTCCAGTCTTGTTCATGTCAGT	1426	CAGGAAACAGCTATGACCGGAAATGAGAGCTACGAA	1547
AE107s4	TGTAAACGACGGCCAGTCTCTGACAGAGCGTCTGTATAC	1427	CAGGAAACAGCTATGACCAAGTCTGTCTACCTTCTG	1548
AE107s5	TGTAAACGACGGCCAGTCTCTTACAGAGCGTCTGTATAC	1428	CAGGAAACAGCTATGACCGTCTGTCTACGCTTCAGAG	1549
AE107s6	TGTAAACGACGGCCAGTCTCTGAGAGCGTCTGTATAC	1429	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACCTG	1550
AE109s1	TGTAAACGACGGCCAGTCTGACGAGTCAATTGAAAGGA	1430	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1551
AE109s2	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1431	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1552
AE109s3	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1432	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1553
AE109s4	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1433	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1554
AE109s5	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1434	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1555
AE109s6	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1435	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1556
AE109s7	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1436	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1557
AE109s8	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1437	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1558
AE109s9	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1438	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1559
AE110s1	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1439	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1560
AE110s10	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1440	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1561
AE110s11	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1441	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1562
AE110s12	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1442	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1563
AE110s2	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1443	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1564
AE110s3	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1444	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1565
AE110s4	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1445	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1566
AE110s5	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1446	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1567
AE110s6	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1447	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1568
AE110s7	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1448	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1569
AE110s8	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1449	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1570
AE110s9	TGTAAACGACGGCCAGTCTGAGAGTCTGAGCAGTGGCC	1450	CAGGAAACAGCTATGACCGTCTGTCTGTCTGTACGCT	1571

Table XII
Sample Description

Race	Cases			Controls			Total
	Angioedema	Angioedema-like	Total	Angioedema	Angioedema-like	Total	
Blacks	11	10	21	32	19	51	72
Caucasians	12	22	34	38	69	107	141
Other	0	1	1	0	1	1	2
Total	23	33	56	70	89	159	215

Table XIII
Candidate Angioedema Susceptibility Genes

Chromosome	Gene	Gene ID
14	Bradykinin B2 Receptor	BDKRB2
19	Tissue Kallikrein	KLK1
X	Aminopeptidase P (Membrane Bound)	XPNPEP2

Table XIV
Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events

Gene ID	SNP ID	Sample or Subgroup	Scores Test	DF	Probability	Estimate Type	A _a ¹	Copies of Rare Allele	Odds Ratio (OR) ²	OR Lower 95% CL	OR Upper 95% CL	p(a) ³
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300	Asymptotic	A,T	1	3.41	1.3238	8.7969	0.28
					0.0251	Exact			3.37	1.2261	10.2718	
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64	1.4211	22.3807	0.09
					0.0062	Exact			5.64	1.2422	34.7611	
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95	1.9838	+INF	0.28
		Angioedema-like	11.39	2	0.0022	Exact		2	10.82	1.3105	+INF	0.22
		Overall	10.72	2	0.0047	Asymptotic		2	11.11	1.2687	97.2709	0.23

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.